

Wed Jun 25 15:53:40 2003

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41; Search time 11.9318 Seconds  
(Without alignments)  
837.928 Million cell updates/sec

Title:

US-09-522-613b-11

Perfect score:

577  
1 SDMLFQKKHLTNTRDVCN.....TFVCENQAPVHFVGVGHC 104

Scoring table:

BROSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

PIR\_73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	95.5	104	2 A39035	ribonuclease-relat
2	287	49.7	111	2 A27121	ribonuclease-relat
3	280.5	48.6	111	1 UX0120	ribonuclease-relat
4	264.5	45.8	111	2 UX0085	pancreatic ribonuc
5	144	25.0	119	2 S41111	pancreatic ribonuc
6	132	22.9	124	1 NRUI	pancreatic ribonuc
7	128	22.2	125	1 A32474	angiogenin (valida
8	126	21.8	128	1 NRCU	pancreatic ribonuc
9	125	21.7	124	1 NRMH	pancreatic ribonuc
10	120	20.3	128	1 NRKS	pancreatic ribonuc
11	120	20.8	128	1 NRGPB	pancreatic ribonuc
12	119.5	20.7	145	1 A35932	angiogenin precurs
13	118	20.5	124	1 NRCB	pancreatic ribonuc
14	117	20.3	128	1 NRCY	pancreatic ribonuc
15	116	20.1	125	1 B43825	angiogenin - rabdi
16	114	19.8	124	1 NRHP	pancreatic ribonuc
17	113	19.6	147	1 NRHOG	angiogenin precurs
18	112	19.4	124	1 NRBOB	pancreatic ribonuc
19	112	19.4	124	1 NRPG	pancreatic ribonuc
20	112	19.4	124	2 JC5560	pancreatic ribonuc
21	112	19.4	124	1 NRPO	pancreatic ribonuc
22	112	19.4	150	1 NRBO	pancreatic ribonuc
23	111.5	19.3	147	2 I52489	ribonuclease 4 (EC
24	111	19.2	124	2 S08549	ribonuclease - dom
25	111	19.2	128	1 NRHO	pancreatic ribonuc
26	111	19.2	167	1 S20066	pancreatic-type ri
27	110.5	19.2	123	1 A43825	angiogenin - pig
28	110.5	19.2	135	1 JC6159	eosinophil-associa
29	110	19.1	124	1 NRGA	pancreatic ribonuc

30	110	19.1	156	2 JC6160	eosinophil-associa
31	109	18.9	124	1 NRSH	pancreatic ribonuc
32	109	18.9	124	1 NRPR	pancreatic ribonuc
33	109	18.9	124	2 S07141	pancreatic ribonuc
34	108	18.7	124	1 NRWB	pancreatic ribonuc
35	108	18.7	124	1 NRGN	pancreatic ribonuc
36	107	18.5	124	1 NRGE	pancreatic ribonuc
37	105	18.2	124	1 NRDEO	pancreatic ribonuc
38	105	18.2	124	1 NRCH	pancreatic ribonuc
39	105	18.2	124	1 NRCHM	pancreatic ribonuc
40	105	18.2	124	1 NRCHB	pancreatic ribonuc
41	105	18.2	128	1 NRCHW	pancreatic ribonuc
42	104	18.0	124	1 NRHY	pancreatic ribonuc
43	103	17.9	124	1 NRDER	pancreatic ribonuc
44	103	17.9	124	1 NRDN	pancreatic ribonuc
45	103	17.9	124	1 NREKN	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C:Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 30-Jun-1993

C:Accession: A39035

R:Ardelet, W.; Mikulski, S.M.; Shogen, K.  
J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e  
A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <AR>

C:Superfamily: pancreatic ribonuclease

Query Match 95.5%; Score 551; DB 2; Length 104;  
Best Local Similarity 96.1%; Pred. No. 2e-48;

Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY	2	DWLTFQKKHLTNTRDVCNNINMSTNLFHCKDKNFIYSRPEPVAKICKIGIASKNVLTTS	61
DB	2	DWLTFQKKHLTNTRDVCNNINMSTNLFHCKDKNFIYSRPEPVAKICKIGIASKNVLTTS	61
QY	62	EFYLSDCVNTSRPCKYKIKLKSTNFCVCENQAPVHFVGVGHC	104
DB	62	EFYLSDCVNTSRPCKYKIKLKSTNFCVCENQAPVHFVGVGSC	104

RESULT 2

A27121

ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Mitte, K.; Sakakibara, F.; Kawachi, H.; Takayan  
Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TIR>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 49.7%; Score 287; DB 2; Length 111;  
Best Local Similarity 49.1%; Pred. No. 7.3e-22;

Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY	2	DWLTFQKKHLTNTRDVCNNINMSTNLF---HCKDKNFIYSRPEPVAKICKIGIASKNV	57
DB	2	NWATFOKKHINTPIINCNTIMDNINIVGCGCKRVNFIISATVATVATCTGVI-NMNV	60



R:Bond, M.D.; Strydom, D.J.  
Biochemistry 28, 6110-6113, 1989  
A:Title: Amino acid sequence of bovine angiotensin  
A:Reference number: A32474; MUID:89375344; PMID:2775757  
A:Accession: A32474  
A:Molecule type: protein  
A:Residues: 1-125 <BON>  
A:Experimental source: Plasma  
R:Meas, P.; Demart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.  
FEBS Lett. 241, 41-45, 1988  
A:Title: The complete amino acid sequence of bovine milk angiotensin.  
A:Reference number: S02001; MUID:89065101; PMID:3197838  
A:Accession: S02001  
A:Molecule type: protein  
A:Residues: 1-125 <MAE>  
A:Experimental source: milk  
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
Submitted to the Brookhaven Protein Data Bank, January 1995  
A:Reference number: A65065; PDB:1AG1  
A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125  
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.  
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995  
A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.  
A:Reference number: A58315; MUID:95224057; PMID:7708754  
A:Contents: annotation; X-ray crystallography, 1.5 angstroms  
R:Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
Submitted to the Brookhaven Protein Data Bank, April 1996  
A:Reference number: A65709; PDB:1GTO  
A:Contents: annotation; conformation by (1)H-NMR, residues 1-125  
R:Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.  
Biochemistry 35, 8870-8880, 1996  
A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spectroscopy  
A:Reference number: A58821; MUID:96280645; PMID:8688423  
A:Contents: annotation; conformation by (1)H-NMR  
R:Reisdorf, C.; Aberer, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.  
Eur. J. Biochem. 224, 811-822, 1999  
A:Title: Proton resonance assignments and secondary structure of bovine angiotensin  
A:Reference number: S48212; MUID:95010071; PMID:7925406  
A:Contents: annotation; conformation by (1)H-NMR  
C:Function:  
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: angiotensin; hydrolase; nucleic acid degradation  
F:60-68/Region: receptor binding status predicted  
F:14,41,119/Active site: His, Lys, His #status predicted  
F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 22.2%; Score 128; DB 1; Length 125;  
Best Local Similarity 34.0%; Pred. No. 7.8e-06;  
Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

OY 16 DVDNNIMSTLNF--HCKDKNTFTYSRPEPKAICKGIASKN-----VLTSSEYL 65  
DB 24 DEYFNMKRRLTRPCKDRFTFHGKNKNDIKAIKCE---DRNGOPYNGDLRISKSEFOI 79  
OY 66 SLC---NYTSR-PCKYKIKSTNFTCYTCENQAPVHF 98  
DB 80 TICHKKGSSRPCKRYGATEDSRIVVGCENGLPVHF 116

RESULT 8  
NRKU  
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)  
N:Alternate names: RNase 1; RNase A  
C:Species: Myocastor coypus (nutria, coypu)  
C:Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
C:Accession: A00822  
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
Biochim. Biophys. Acta 453, 400-409, 1976  
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
A:Reference number: A90612; MUID:77065676; PMID:999896  
A:Accession: A00822  
A:Molecule type: protein

A:Residues: 1-128 <VAN>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.8%; Score 126; DB 1; Length 128;  
Best Local Similarity 29.9%; Pred. No. 1.3e-05;  
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

OY 6 FQKKHL-----TNRDVCNNIM-STNLF--HCKDKNTFTYSRPEPKAICKGIASKN 57  
DB 8 FERQHMDSRGSPTNPVNCNEMKSRMNTQGRCKPVTVEHPLADVOAVC-----FQKNV 63  
OY 58 L-----TTSEFLSDCNYTSRP---CKYKIKKSTNFTCYTCENQ--APVHF 98  
DB 64 LCKNGQTCYOSNSNMHITDCRVTNSDYPNCISRTSOEKSIVVACENGPVPHF 120

RESULT 9  
NRMK  
pancreatic ribonuclease (EC 3.1.27.5) - minke whale  
N:Alternate names: RNase 1; RNase A  
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
C:Accession: A00818  
R:Emmens, M.; Welling, G.W.; Beintema, J.J.  
Biochem. J. 157, 317-323, 1976  
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease  
A:Reference number: A00818; MUID:76277855; PMID:962870  
A:Accession: A00818  
A:Molecule type: protein  
A:Residues: 1-124 <EMW>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 21.7%; Score 125; DB 1; Length 124;  
Best Local Similarity 28.6%; Pred. No. 1.6e-05;  
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

OY 4 LTFQKHLLTNRDVC-----CNNIMSTNLF--HCKDKNTFTYSRPEPKAICKGIASKN 55  
DB 6 MKFQROHNDSCNSPCNNPNYCNQMMRRKMTQGRCKPVTVEHSELEVKAVC-----SQK 61  
OY 56 NVL-----TTSEFLSDCNYTSRP---CKYKIKKSTNFTCYTCENQ--APVHF 98  
DB 62 NVLCKNGRTNCEESNTPMHTIDCRQTSRKYPCAYKTSQKEKHLIVACEENPVVPHF 120

RESULT 10  
NRKS  
pancreatic ribonuclease (EC 3.1.27.5) - castroagua  
C:Species: Proechimys guirae (castroagua)  
C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 30-Sep-1993  
C:Accession: A00821  
R:Beintema, J.J.; Knol, G.; Martena, B.  
Biochim. Biophys. Acta 705, 102-110, 1982  
A:Title: The primary structures of pancreatic ribonucleases from African porcupine and  
A:Reference number: A90644; MUID:83000399; PMID:7115727  
A:Accession: A00821  
A:Molecule type: protein  
A:Residues: 1-128 <BEI>  
A:Note: residues 67-78 were positioned primarily by homology with other ribonucleases  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

2: Superfamily: pancreatic ribonuclease



